

Methods for Single Cell Analysis of the Epigenome, Transcriptome, and Genome

Summary (1024-character limit)

There are currently no methodologies that allow for epigenome, genome and transcriptome analysis all in a single cell. In addition, there are currently no methodologies that permit repeating the results of these analyses on the same single cells. Scientists at the National Cancer Institute (NCI) Laboratory of Cellular Oncology have developed a method for generating a "reusable" single cell that allows for repeated experiments on the same cell. Utilizing this methodology epigenomic, genomic, and transcriptomic analysis can be performed on the same cell. NCI seeks parties to license or co-develop the technology through research collaborations.

NIH Reference Number

E-069-2017

Product Type

Diagnostics

Keywords

• Single Cell Analysis, Epigenomic, Genomic, Transcriptomic, Diagnostic, Research Tool, Tosato

Collaboration Opportunity

This invention is available for licensing and co-development.

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Description of Technology

There are currently no methodologies that allow for epigenome, genome and transcriptome analysis all in a single cell. In addition, there are currently no methodologies that permit repeating the results of these analyses on the same single cells.

Scientists at the National Cancer Institute (NCI) Laboratory of Cellular Oncology have developed a method for generating a "reusable" single cell by crosslinking cellular proteins and DNA to a polyacrylamide scaffold, thus preserving the proteins and genomic DNA in their location even after repeated experiments on the same cell. Given the reusability of the cell, each experiment can be repeated multiple times, and statistical analysis can be applied to validate the results from single cells. Methods for



detecting epigenetic changes using this methodology are also disclosed.

Potential Commercial Applications

- Research Tool
- Diagnostic Assays

Competitive Advantages

• The ability to "reuse" a single cell overcomes major issues that currently impair single cell analysis, such as analyzing multiple epigenetic modifications, lack of reproducibility controls, and statistical analysis

Inventor(s)

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Development Stage

• Basic (Target Identification)

Patent Status

• U.S. Provisional: U.S. Provisional Patent Application Number 62/502,247, Filed 05 May 2017

Therapeutic Area

Cancer/Neoplasm